

RAW SEQUENCE LISTING ERROR REPORT

BIOTEC. OLOGY
SYSTEMS
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JUN 26 2001

1600/290



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/748,127

Source: 1646

Date Processed by STIC: 6-6-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/748,127

DATE: 06/06/2001

TIME: 12:44:03

Input Set : A:\Seqlist.txt

Output Set: C:\CRF3\06062001\I748127.raw

4 <110> APPLICANT: YAN, Chunhua et al
 6 <120> TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
 7 PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
 8 DRUG-METABOLIZING PROTEINS,
 9 AND USES THEREOF
 12 <130> FILE REFERENCE: CL000685
 14 <140> CURRENT APPLICATION NUMBER: 09/748,127
 15 <141> CURRENT FILING DATE: 2000-12-27
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

150 <210> SEQ ID NO: 3

151 <211> LENGTH: 504

152 <212> TYPE: DNA

153 <213> ORGANISM: Human

155 <220> FEATURE:

156 <221> NAME/KEY: misc_feature

157 <222> LOCATION: (1)...(504)

158 <223> OTHER INFORMATION: n = A,T,C or G

160 <400> SEQUENCE: 3

E--> 161 meatgtwall lalalilllt lalsgtrarg hlppgptlp llnllqlrp galysglmrl 60
 E--> 162 skkygvpvfti ylgpwrpvvv lvgqavrea lggqaeefsg rgtvamlegt fdghgvffsn 120
 E--> 163 gerwrqlrkf tmlalrdlqm gkregeeliq aearclvetf qgtegrpfdp slllaqatsn 180
 E--> 164 vvcslifglr fsyedkefqa vvraaggtil gvssqggqty emfswflrpl pgphkqlhh 240
 E--> 165 vstlaaftvr qvqqhqnld asgpardlvd aflkmaqee qnpgteftnk nmlmtviyil 300
 E--> 166 fagtmtvstt vgytllllmk yphvqkwre elnrelgagq apslgdrtrl pytdavlhea 360
 E--> 167 qrllalvpmg iprtlmrttr frgytlpqgt evfpllgsl hdpnifkhpe efnpdrflda 420
 E--> 168 dgrfrkheaf lpfslgkrvc lgeglakael flfftilqa fslespcppd tllskptvsg 480
 E--> 169 lfnippafql qvrptdlhst tqtr 504

*This is listed as a DNA sequence.
 There are invalid nucleic acid designators
 in the sequence. There can be no
 single letter amino acids in a DNA
 sequence. Please review and
 correct.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/748,127

DATE: 06/06/2001

TIME: 12:44:04

Input Set : A:\Seqlist.txt

Output Set: C:\CRF3\06062001\I748127.raw

L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:161 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:29
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:162 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:163 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:26
L:164 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:24
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:165 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:23
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:166 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:167 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:29
L:168 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:28
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:169 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12